STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
   ## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: /0/552,909A
Source: /FWD
Date Processed by STIC: /1/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

2_____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
       Numbering   use space characters, instead.

4_____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                          ensure your subsequent submission is saved in ASCII text.

5_____Variable Length   Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                          each n or Xaa can only represent a single residue. Please present the maximum number of each
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                          previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                          the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                          Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
       (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                          (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                          This sequence is intentionally skipped
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
       (NEW RULES)   <210> sequence id number
                          <400> sequence id number
                          000

9_____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
        Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                          is Artificial Sequence. (see item 11 below)

11_____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
                          of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
                          Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
                          explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
                          Sequence Rules

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
        "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                          listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING   DATE: 11/07/2006
PATENT APPLICATION: US/10/552,909A   TIME: 11:51:44

        Input Set : N:\RJAVED\10552909A.txt
        Output Set: N:\CRF4\11072006\J552909A.raw

see item 4 on Erra summary sheet

see pp 1,3—4

Does Not Comply
Corrected Diskette Needed

```
   3 <110> APPLICANT: Xiao, Yingxao
   4        Feng, Xin-Hua
   6 <120> TITLE OF INVENTION: Gene expression suppression agents
   8 <130> FILE REFERENCE: 132848-01US
  10 <140> CURRENT APPLICATION NUMBER: US 10/552,909A
  11 <141> CURRENT FILING DATE: 2005-10-13
  13 <160> NUMBER OF SEQ ID NOS: 9
  15 <210> SEQ ID NO: 1
  16 <211> LENGTH: 27
  17 <212> TYPE: DNA
  18 <213> ORGANISM: Human
  20 <220> FEATURE:
  21 <221> NAME/KEY: primer_bind
  22 <223> OTHER INFORMATION: Primer to amplify upstream promoter containing Box D in the
  23        Human 5S RNA gene
  25 <310> PATENT DOC NO: PCT/US2003/014631
  26 <311> PATENT FILING DATE: 2003-05-12
  27 <312> PUBLICATION DATE: PCT WO 2004/106488 A2
  29 <400> SEQUENCE: 1
  30 aacggatcca aaacgctgcc tccgcga   27
  32 <210> SEQ ID NO: 2
  33 <211> LENGTH: 25
  34 <212> TYPE: DNA
  35 <213> ORGANISM: Human
  37 <220> FEATURE:
  38 <221> NAME/KEY: primer_bind
  39 <223> OTHER INFORMATION: Downstream reverse primer used to amplify the upstream
  40        promoter containing Box D in the Human 5S RNA gene. The
  41        sequence contains a Pst1 site at 7 bp upstream of the
  42        transcription site.
  44 <400> SEQUENCE: 2
  45 tagacgctgc aggaggcgcc tggct   25
  51 <210> SEQ ID NO: 3
  52 <211> LENGTH: 269
  53 <212> TYPE: DNA
  54 <213> ORGANISM: Human
  56 <220> FEATURE:
  57 <221> NAME/KEY: promoter
  58 <223> OTHER INFORMATION: Calculated BamHI-PstI fragment of the upstream promoter
  59        containing Box D in the Human 5S gene. Cloned into
  60        pBluescript-KS to give plasmid pPPVI.
  62 <400> SEQUENCE: 3
  63 ggatccaaaa cgctgcctcc gcgacagggc ggaggacgga gggcgtccca ggatcgtggg 60
```

<300> *insert this numeric identifier at the beginning of publication information. It never has a response.*

<312>

this is for Publication Date use this format; yyyy-mm-dd

since this is a patent current number, change to 3/07

W—> 25

W—> 27

```
 65 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
 67 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc gggggtcccc gatccgagcc 180
 69 ccgcggcccc gggctggcgg tgtcggctgc aatccggcgg gcacggccgg ccgggctggg 240
 71 ctcttggggc agccaggcgc ctccttcag 269
 73 <210> SEQ ID NO: 4
 74 <211> LENGTH: 84
 75 <212> TYPE: DNA
 76 <213> ORGANISM: Human
 78 <220> FEATURE:
 79 <221> NAME/KEY: terminator
 80 <223> OTHER INFORMATION: Comprises Box A, C and terminator of the human 5S RNA gene.
 81      Serves as a top strand to anneal with SEQ ID NO: 5 to
 82      create a double-stranded DNA molecule.
 84 <400> SEQUENCE: 4
 86 agaagacgaa gctaagcagg gtcgggcctg gttagtactt ggatgggaga ccgcctggga 60
 88 ataccgggtg ctgtaggctt tttg 84
 91 <210> SEQ ID NO: 5
 92 <211> LENGTH: 88
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Human
 96 <220> FEATURE:
 97 <221> NAME/KEY: terminator
 98 <223> OTHER INFORMATION: Comprises Box A, C and terminator of the human 5S RNA gene.
 99      Serves as a top strand to anneal with SEQ ID NO: 4 to
100      create a double-stranded DNA molecule.
102 <400> SEQUENCE: 5
103 tcgacaaaaa gcctacagca cccggtattc ccaggcggtc tcccatccaa gtactaacca 60
105 ggcccgaccc tgcttagctt cgtcttct 88
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 367
110 <212> TYPE: DNA
111 <213> ORGANISM: Human
113 <220> FEATURE:
114 <221> NAME/KEY: promoter
115 <223> OTHER INFORMATION: A BamHI-SalI fragment of plasmid pPPV2 containing the
116      upstream promoter containing Box D, A, C and the terminator
117      of the Human 5S gene.
119 <400> SEQUENCE: 6
120 ggatccaaaa cgctgcctcc gcgacagggc ggaggacgga gggcgtccca ggatcgtggg 60
122 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
124 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc gggggtcccc gatccgagcc 180
126 ccgcggcccc gggctggcgg tgtcggctgc aatccggcgg gcacggccgg ccgggctggg 240
128 ctcttggggc agccaggcgc ctccttcagg aattcgatag aagacgaagc taagcagggt 300
130 cgggcctggt tagtacttgg atgggagacc gcctgggaat accgggtgctg taggctttt 360
132 tgtcgac 367
134 <210> SEQ ID NO: 7
135 <211> LENGTH: 51
136 <212> TYPE: DNA
137 <213> ORGANISM: Human
```

```
139 <220> FEATURE:
140 <221> NAME/KEY: misc_RNA
141 <223> OTHER INFORMATION: Contains designed siRNA sequence. Serves as a top strand
142       to anneal with SEQ ID NO: 8 to create a double-stranded DNA
143       molecule with PstI at the 5' end and BbsI at the 3' end.
145 <400> SEQUENCE: 7
146 gcnnnnnnnn nnnnnnnnnn ttttcggnnn nnnnnnnnnn nnnnnntttt t 51
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 59
151 <212> TYPE: DNA
152 <213> ORGANISM: Human
154 <220> FEATURE:
155 <221> NAME/KEY: misc_RNA
156 <223> OTHER INFORMATION: Contains designed siRNA sequence. Serves as a top strand
157       to anneal with SEQ ID NO: 7 to create a double-stranded DNA
158       molecule with PstI at the 5' end and BbsI at the 3' end.
160 <400> SEQUENCE: 8
161 agctaaaaag nnnnnnnnnn nnnnnnnncc gaaannnnnn nnnnnnnnnn nnngctgca 59
163 <210> SEQ ID NO: 9
164 <211> LENGTH: 399
165 <212> TYPE: DNA
166 <213> ORGANISM: Human
168 <220> FEATURE:
169 <221> NAME/KEY: misc_structure
170 <223> OTHER INFORMATION: A BamHI-SalI fragment of plasmid pPPV2 containing the siRNA
171       design. The second stretch of the 19 "n" bases are
172       complementary and reverse to the first stretch.
174 <400> SEQUENCE: 9
175 ggatccaaaa cgctgcctcc gcgacagggc ggaggacgga gggcgtccca ggatcgtggg 60
177 ccctgggcct gacgcctcgg agcactccct gctccgagcg ggcccgatgt ggtggaagct 120
179 cgggagcgcg ggagccgggg gaaggccgcg ggcagccgtc gggggtcccc gatccgagcc 180
181 ccgcggcccc gggctggcgg tgtcggctgc aatccggcgg gcacggccgg ccgggctggg 240
183 ctcttggggc agccaggcgc ctccttcagc nnnnnnnnnn nnnnnnnnnt ttcggnnnnn 300
185 nnnnnnnnnn nnnnttttta gctaagcagg gtcgggcctg gttagtactt ggatgggaga 360
187 ccgcctggga ataccgggtg ctgtaggctt tttgtcgac 399
```

W--> 146

W--> 161

W--> 183

Handwritten annotations:

n's need explanation. See p. 4 for error explanation.

see p. 4

← OK, but all the n's need explanation, further.

Which bases do these n's represent?

FYI: all nucleotides MUST be in lower-case letter

(see 1.823 of Sequence Rules) and p.4

VARIABLE LOCATION SUMMARY   DATE: 11/07/2006
PATENT APPLICATION: US/10/552,909A   TIME: 11:51:45

Input Set : N:\RJAVED\10552909A.txt
Output Set: N:\CRF4\11072006\J552909A.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:7; N Pos. 3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,28,29,30
Seq#:7; N Pos. 31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:8; N Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,35
Seq#:8; N Pos. 36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53
Seq#:9; N Pos. 271,272,273,274,275,276,277,278,279,280,281,282,283,284,285
Seq#:9; N Pos. 286,287,288,289,296,297,298,299,300,301,302,303,304,305,306
Seq#:9; N Pos. 307,308,309,310,311,312,313,314

VERIFICATION SUMMARY   DATE: 11/07/2006
PATENT APPLICATION: US/10/552,909A   TIME: 11:51:45

Input Set : N:\RJAVED\10552909A.txt
Output Set: N:\CRF4\11072006\J552909A.raw

```
L:25 M:284 W: Blank Line not Allowed, <310> field identifier
L:27 M:256 W: Invalid Numeric Header Field, Wrong PUBLICATION DATE:YYYY-MM-DD
L:146 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:161 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:183 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:240
L:183 M:112 C: (48) String data converted to lower case,
M:341 Repeated in SeqNo=9
```